

**PALM INTRANET**Day : Monday  
Date: 1/14/2008

Time: 20:29:26

**Inventor Name Search**

10/539,178

Enter the **first few letters** of the Inventor's Last Name.Additionally, enter the **first few letters** of the Inventor's First name.**Last Name****First Name**

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**PALM INTRANET**Day : Monday  
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## Inventor Name Search

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Time: 20:29:26

## Inventor Name Search

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**Last Name****First Name**

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# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150537\_us-10-539-178-1.rng.

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GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 290 Seconds  
(without alignments)  
745.652 Million cell updates/sec

Title: US-10-539-178-1  
Perfect score: 20  
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_200711:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000:\*
- 4: geneseqn2001a:\*
- 5: geneseqn2001b:\*
- 6: geneseqn2002a:\*
- 7: geneseqn2002b:\*
- 8: geneseqn2003a:\*
- 9: geneseqn2003b:\*
- 10: geneseqn2003c:\*
- 11: geneseqn2003d:\*
- 12: geneseqn2004a:\*
- 13: geneseqn2004b:\*
- 14: geneseqn2004c:\*
- 15: geneseqn2004d:\*

```

16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
19: geneseqn2006a:*
20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	13	ADQ13606	Adq13606 DMD regio
c 2	18.4	92.0	886	14	AGE30203	Age30203 Human sin
c 3	18.4	92.0	85869	15	AFI70361	Afi70361 Human gen
c 4	18.4	92.0	85878	15	AFI74665	Afi74665 Human gen
5	17.4	87.0	101365	16	AEP71437	Aep71437 Alzheimer
6	17.4	87.0	101365	21	AGA38905	Aga38905 Alzheimer
7	17.4	87.0	172781	17	AED89385	Aed89385 Human bre
c 8	17	85.0	1189	14	AEX05694	Aex05694 Bovine sp
c 9	17	85.0	1189	14	AEW40747	Aew40747 Bovine sp
10	16.8	84.0	201	14	AEX54475	Aex54475 Human rhe
11	16.8	84.0	201	14	AEX54472	Aex54472 Human rhe
c 12	16.8	84.0	544	4	AAK10343	Aak10343 Human bra
c 13	16.8	84.0	544	4	ABA62026	Aba62026 Human foe
c 14	16.8	84.0	544	4	AAI41964	Aai41964 Probe #10
c 15	16.8	84.0	544	4	ABS35926	Abs35926 Human liv
c 16	16.8	84.0	544	4	ABA29497	Aba29497 Probe #79
c 17	16.8	84.0	544	4	AAK36244	Aak36244 Human bon
c 18	16.8	84.0	544	4	AAI17257	Aai17257 Probe #71
c 19	16.8	84.0	544	6	ABS10337	Abs10337 Human gen
c 20	16.8	84.0	545	14	AGE91644	Age91644 Human sin
c 21	16.8	84.0	545	14	AGE84880	Age84880 Human sin
c 22	16.8	84.0	546	14	AGE32574	Age32574 Human sin
23	16.8	84.0	551	14	AGE32930	Age32930 Human sin
24	16.8	84.0	551	15	AGE32931	Age32931 Human sin
25	16.8	84.0	553	14	AGE32573	Age32573 Human sin
c 26	16.8	84.0	569	14	AGH48999	Agh48999 Human sin
27	16.8	84.0	584	14	AGG06871	Agg06871 Human sin
28	16.8	84.0	658	14	AGH02802	Agh02802 Human sin
29	16.8	84.0	658	15	AGH02801	Agh02801 Human sin
30	16.8	84.0	1334	14	AGG32845	Agg32845 Human sin
31	16.8	84.0	1370	1	AAN82410	Aan82410 Plasmid p
32	16.8	84.0	1370	10	ADB52335	Adb52335 Primary r
33	16.8	84.0	1626	22	AFQ96317	Afq96317 Rat type
34	16.8	84.0	2266	8	ABT41702	Abt41702 Toxicity
35	16.8	84.0	2266	10	ADB52339	Adb52339 Primary r
36	16.8	84.0	2266	13	ADV40787	Adv40787 Rat card
c 37	16.8	84.0	3218	5	ABL06670	Abl06670 Drosophil
c 38	16.8	84.0	3218	17	AFB87203	Afb87203 Fruit fly
39	16.8	84.0	16922	18	AGD78652	Agd78652 Human gen
40	16.8	84.0	16923	18	AGD78689	Agd78689 Human gen
41	16.8	84.0	30057	11	ACN44664	Acn44664 Mouse gen
c 42	16.8	84.0	50000	9	ADC56844	Adc56844 Human ATP
c 43	16.8	84.0	56423	8	ADC85728	Adc85728 Human GPC
c 44	16.8	84.0	73063	13	ADQ97727	Adq97727 Human can

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150537\_us-10-539-178-187.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 319 Seconds  
(without alignments)  
745.652 Million cell updates/sec

Title: US-10-539-178-187  
Perfect score: 22  
Sequence: 1 cactgtgctattctggtttggaa 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_200711:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000:  
4: geneseqn2001a:  
5: geneseqn2001b:  
6: geneseqn2002a:  
7: geneseqn2002b:  
8: geneseqn2003a:  
9: geneseqn2003b:  
10: geneseqn2003c:  
11: geneseqn2003d:  
12: geneseqn2004a:  
13: geneseqn2004b:  
14: geneseqn2004c:  
15: geneseqn2004d:

```

16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
19: geneseqn2006a:*
20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
						%
1	22	100.0	22	13	ADQ13792	Adq13792 DMD regio
c 2	17.8	80.9	1510	8	ADK59908	Adk59908 Plant DNA
c 3	17.8	80.9	1510	8	ADK56233	Adk56233 Plant DNA
4	17.8	80.9	2805	15	AFO56327	Afo56327 Glycine m
5	17.4	79.1	601	15	AFJ20862	Afj20862 Human DNA
c 6	17.4	79.1	163662	15	AFI70889	Afi70889 Human gen
c 7	17.4	79.1	163664	15	AFI71890	Afi71890 Human gen
8	17.2	78.2	601	15	AFJ12221	Afj12221 Human DNA
c 9	17.2	78.2	700	4	AAH93101	Aah93101 Human inf
c 10	17.2	78.2	859	14	AGE58571	Age58571 Human sin
11	17.2	78.2	1085	14	AEW90937	Aew90937 Bovine sp
12	17.2	78.2	1085	14	AEW25991	Aew25991 Bovine sp
c 13	17.2	78.2	2006	14	AEW79027	Aew79027 Bovine sp
c 14	17.2	78.2	2006	14	AEW14081	Aew14081 Bovine sp
15	17.2	78.2	2335	9	ADB62550	Adb62550 Human cDN
16	17.2	78.2	2885	12	ADX50184	Adx50184 Plant ful
17	17.2	78.2	3056	19	AFC58776	Afc58776 Maize cDN
18	17.2	78.2	3234	20	AFK73017	Afk73017 Polymorph
19	17.2	78.2	3941	14	AEW75798	Aew75798 Bovine sp
20	17.2	78.2	3941	14	AEW10852	Aew10852 Bovine sp
21	17.2	78.2	10118	22	AFB68168	Afb68168 Mouse kin
22	17.2	78.2	30072	11	ACN44152	Acn44152 Mouse gen
23	17.2	78.2	75176	15	AFI71644	Afi71644 Human gen
24	17.2	78.2	83784	16	AEP71425	Aep71425 Alzheimer
25	17.2	78.2	83784	20	AGA38893	Aga38893 Alzheimer
26	17.2	78.2	110000	11	ACN44934_2	Continuation (3 of
c 27	17.2	78.2	110000	13	ABD32780_3	Continuation (4 of
28	17.2	78.2	110000	15	AFI71517_1	Continuation (2 of
29	17.2	78.2	110000	16	ADZ46976_4	Continuation (5 of
c 30	17.2	78.2	187136	15	AFI75575	Afi75575 Human gen
c 31	17.2	78.2	294575	16	AEA61217	Aea61217 Human STK
c 32	17.2	78.2	313287	13	ABD33100	Abd33100 Human can
c 33	17.2	78.2	313287	19	AEJ13040	Aej13040 Cancer-as
c 34	17	77.3	2865	19	AEH40248	Aeh40248 Cryptospo
35	16.8	76.4	282	3	AAA44291	Aaa44291 Human sec
c 36	16.8	76.4	492	15	AGG56864	Agg56864 Human sin
c 37	16.8	76.4	492	15	AGG56863	Agg56863 Human sin
c 38	16.8	76.4	501	22	AER72552	Aer72552 Bovine tr
39	16.8	76.4	549	8	ACF56843	Acf56843 Rice leaf
40	16.8	76.4	652	14	AGF26732	Agf26732 Human sin
41	16.8	76.4	887	14	AGE34784	Age34784 Human sin
42	16.8	76.4	887	14	AGE34785	Age34785 Human sin
43	16.8	76.4	887	15	AGE34786	Age34786 Human sin
c 44	16.8	76.4	996	14	AEW65527	Aew65527 Bovine sp

# **SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150537\_us-10-539-178-188.rng.**

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 347 Seconds  
(without alignments)  
745.652 Million cell updates/sec

Title: US-10-539-178-188  
Perfect score: 24  
Sequence: 1 tttatgcttcttgcaaactactg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_200711:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000:\*

4: geneseqn2001a:\*

5: geneseqn2001b:\*

6: geneseqn2002a:\*

7: geneseqn2002b:\*

8: geneseqn2003a:\*

9: geneseqn2003b:\*

10: geneseqn2003c:\*

11: geneseqn2003d:\*

12: geneseqn2004a:\*

13: geneseqn2004b:\*

14: geneseqn2004c:\*

15: geneseqn2004d:\*

```

16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
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20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
						%
1	24	100.0	24	13	ADQ13793	Adq13793 DMD regio
2	22.4	93.3	601	15	AFK48071	Afk48071 Human DNA
3	22.4	93.3	197131	15	AFI71019	Afi71019 Human gen
4	22.4	93.3	197132	15	AFI75514	Afi75514 Human gen
5	19.2	80.0	600	17	AFI41012	Afi41012 Chicken s
6	19.2	80.0	600	17	AFI41010	Afi41010 Chicken s
7	19.2	80.0	600	17	AFI41011	Afi41011 Chicken s
8	19.2	80.0	1493	19	AEL26508	Ael26508 Human cDN
9	19.2	80.0	2966	19	AEJ45416	Aej45416 Human G p
10	19.2	80.0	2970	16	ADY17168	Ady17168 DNA encod
11	18.8	78.3	514	10	ADE81377	Ade81377 Arabidops
c 12	18.8	78.3	539	6	ABN62278	Abn62278 Human can
c 13	18.8	78.3	539	16	ACL58171	Acl58171 Human col
c 14	18.8	78.3	539	17	AGD43119	Agd43119 Human pol
15	18.8	78.3	3453	20	AFY34287	Afy34287 Saccharom
16	18.8	78.3	3453	21	AGB18665	Agb18665 Saccharom
c 17	18.4	76.7	912	8	ACF72332	Acf72332 Staphyloc
c 18	18.4	76.7	1578	2	AAV74527	Aav74527 Staphyloc
19	18.2	75.8	57	6	ABN84050	Abn84050 Glutamate
20	18.2	75.8	99	6	ABN84035	Abn84035 Single ch
c 21	18.2	75.8	570	12	ADL87078	Adl87078 DNA up-re
c 22	18.2	75.8	570	12	ADL87077	Adl87077 DNA up-re
c 23	18.2	75.8	600	14	AEW61711	Aew61711 Bovine sp
c 24	18.2	75.8	600	14	AEV96764	Aev96764 Bovine sp
c 25	18.2	75.8	601	15	AFJ99780	Afj99780 Human DNA
26	18.2	75.8	633	22	AEM76588	Aem76588 Soybean (
c 27	18.2	75.8	675	13	AET08474	Aet08474 C. albica
c 28	18.2	75.8	931	14	AEX00449	Aex00449 Bovine sp
c 29	18.2	75.8	931	14	AEW35502	Aew35502 Bovine sp
c 30	18.2	75.8	1355	14	AEW67443	Aew67443 Bovine sp
c 31	18.2	75.8	1355	14	AEW02497	Aew02497 Bovine sp
32	18.2	75.8	1371	5	AAS76855	Aas76855 DNA encod
c 33	18.2	75.8	8450	13	ADR84479	Adr84479 Aspergill
34	18.2	75.8	236964	15	AFI74097	Afi74097 Human gen
35	17.8	74.2	200	15	AFP47448	Afp47448 Glycine m
36	17.8	74.2	384	10	ADF57738	Adf57738 Human pol
c 37	17.8	74.2	586	13	ACN45257	Acn45257 Cotton pr
c 38	17.8	74.2	600	18	AFU84500	Afu84500 Human pro
39	17.8	74.2	803	14	AGG01762	Agg01762 Human sin
40	17.8	74.2	803	14	AGG01763	Agg01763 Human sin
41	17.8	74.2	2280	13	ADQ22219	Adq22219 Human sof
42	17.8	74.2	2646	5	ABL07099	Ab107099 Drosophil
43	17.8	74.2	2646	17	AFB87846	Afb87846 Fruit fly
44	17.8	74.2	2655	10	ADM02480	Adm02480 Human cDN

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150537\_us-10-539-178-2.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 347 Seconds  
(without alignments)  
745.652 Million cell updates/sec

Title: US-10-539-178-2  
Perfect score: 24  
Sequence: 1 tcatgtgttagttctatcgcaaa 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_200711:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000:\*

4: geneseqn2001a:\*

5: geneseqn2001b:\*

6: geneseqn2002a:\*

7: geneseqn2002b:\*

8: geneseqn2003a:\*

9: geneseqn2003b:\*

10: geneseqn2003c:\*

11: geneseqn2003d:\*

12: geneseqn2004a:\*

13: geneseqn2004b:\*

14: geneseqn2004c:\*

15: geneseqn2004d:\*

```

16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
19: geneseqn2006a:*
20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
						%
1	24	100.0	24	13	ADQ13607	Adq13607 DMD regio
c 2	24	100.0	132	2	AAQ66654	Aaq66654 Fragment
c 3	18.2	75.8	1039	15	AFO98879	Afo98879 Glycine m
c 4	18.2	75.8	130130	19	AEM23543	Aem23543 Human TAT
c 5	18.2	75.8	163022	15	AFI74859	Afi74859 Human gen
6	18.2	75.8	221600	16	ADX80720	Adx80720 Human neu
7	17.6	73.3	399	10	ACH48970	Ach48970 Human leu
8	17.6	73.3	507	7	ADW41630	Adw41630 cDNA elev
9	17.6	73.3	507	7	ADS72776	Ads72776 Human kid
c 10	17.6	73.3	549	2	AAT83808	Aat83808 DNA encod
11	17.6	73.3	601	15	AFK53912	Afk53912 Human DNA
12	17.6	73.3	601	15	AFI97130	Afi97130 Human DNA
13	17.6	73.3	645	6	AAS61746	Aas61746 Lung smal
14	17.6	73.3	645	8	ADD66935	Add66935 Human lun
15	17.6	73.3	645	10	ADE88189	Ade88189 Human lun
16	17.6	73.3	927	14	AEW77568	Aew77568 Bovine sp
17	17.6	73.3	927	14	AEW12622	Aew12622 Bovine sp
18	17.6	73.3	946	5	AAI97773	Aai97773 Human neu
19	17.6	73.3	1400	18	AFU82077	Afu82077 Human pro
c 20	17.6	73.3	1597	13	ADO60399	Ado60399 (R)-hydro
c 21	17.6	73.3	1609	13	ADO60400	Ado60400 (R)-hydro
c 22	17.6	73.3	1632	6	AAF88779	Aaf88779 P. amygd
c 23	17.6	73.3	1632	16	AEC39603	Aec39603 Almond hy
c 24	17.6	73.3	1680	19	AEH91897	Aeh91897 Prunus du
c 25	17.6	73.3	1680	19	AEH91900	Aeh91900 Prunus du
26	17.6	73.3	2000	8	ACL36093	Acl36093 Rice stre
c 27	17.6	73.3	2162	6	AAF88778	Aaf88778 Almond md
c 28	17.6	73.3	2162	16	AEC39601	Aec39601 Almond hy
29	17.6	73.3	2241	8	ADG10551	Adg10551 Human STA
30	17.6	73.3	2494	4	AAS31100	Aas31100 Human dia
31	17.6	73.3	2690	4	AAH14245	Aah14245 Human cDN
32	17.6	73.3	2815	2	AAZ77532	Aaz77532 Human ova
33	17.6	73.3	3056	13	ADO35558	Ado35558 Novel mou
34	17.6	73.3	3172	12	ADL12671	Adl12671 Human ste
35	17.6	73.3	3791	10	ADG77060	Adg77060 Human nuc
36	17.6	73.3	3803	8	ADG10859	Adg10859 Human STA
37	17.6	73.3	3803	17	AED18337	Aed18337 Fibrotic
38	17.6	73.3	3815	8	ADG10553	Adg10553 Human STA
39	17.6	73.3	3817	15	AFI63896	Afi63896 Human cDN
40	17.6	73.3	3835	15	AFI59411	Afi59411 Human cDN
41	17.6	73.3	3835	17	AED14299	Aed14299 Human cum
42	17.6	73.3	3835	17	AFU76842	Afu76842 Human pro
43	17.6	73.3	3839	4	AAF32759	Aaf32759 Human sec
44	17.6	73.3	3839	8	ABZ73486	Abz73486 Secreted

# SCORE Search Results Details for Application : Result 20080109\_150539\_us-10-53

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This page gives you Search Results detail for the Application 10539178 and Search Result 20080109\_150539\_us-10-53.

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1145 Seconds  
(without alignments)  
1429.452 Million cell updates/sec

Title: US-10-539-178-1  
Perfect score: 20  
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_env:  
2: gb\_pat:  
3: gb\_ph:  
4: gb\_pl:  
5: gb\_pr:  
6: gb\_ro:  
7: gb\_sts:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vi:  
11: gb\_ov:  
12: gb\_in:  
13: gb\_om:  
14: gb\_ba:  
15: gb\_htg1:  
16: gb\_htg2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
	1	20	100.0	1387	5	HUMMDMDPR
	2	20	100.0	11747	5	AF276053S1
c	3	20	100.0	133889	5	AL031643
c	4	20	100.0	185393	5	CR956355
	5	19	95.0	913	7	BV473540
c	6	19	95.0	42246	5	Z82253
	7	19	95.0	178717	5	AC194803
	8	19	95.0	182897	16	AL158202
c	9	18.4	92.0	754	7	BV499640
c	10	18.4	92.0	1545	12	AK223668
	11	18.4	92.0	52720	15	AC107997
	12	18.4	92.0	62019	5	AC105239
c	13	18.4	92.0	83767	5	AC114307
	14	18.4	92.0	110000	12	AM055943_18
c	15	18.4	92.0	117100	5	AC137741
c	16	18.4	92.0	125535	5	AC073385
	17	18.4	92.0	129361	5	AL603789
	18	18.4	92.0	134124	5	AL160266
c	19	18.4	92.0	134580	15	AC025359
	20	18.4	92.0	138740	5	AC008063
	21	18.4	92.0	139409	5	AC069181
c	22	18.4	92.0	142557	5	AL356499
	23	18.4	92.0	144200	15	AC022638
c	24	18.4	92.0	152304	15	AC023032
	25	18.4	92.0	158699	5	AP006183
	26	18.4	92.0	158852	15	AC023023
c	27	18.4	92.0	162063	16	AC156381
c	28	18.4	92.0	166215	5	CT826194
c	29	18.4	92.0	167876	16	AC156384
	30	18.4	92.0	171131	5	AC191957
	31	18.4	92.0	173065	6	AC116740
c	32	18.4	92.0	174926	5	CT998538
	33	18.4	92.0	176032	5	AC194673
	34	18.4	92.0	183903	15	AC020684
	35	18.4	92.0	184470	5	AC187130
	36	18.4	92.0	185859	15	AC068026
c	37	18.4	92.0	188873	5	AC193035
	38	18.4	92.0	205673	6	AC126688
	39	18.4	92.0	212598	6	AC158898
c	40	18.4	92.0	223953	15	AC122973
c	41	18.4	92.0	226284	6	AC099609
	42	18.4	92.0	227181	15	AC121010
	43	18.4	92.0	237143	15	AC073769
	44	18.4	92.0	237450	15	AC095092
	45	18.4	92.0	240486	15	AC095305

## ALIGNMENTS

## RESULT 1

HUMMDMDPR

LOCUS HUMMDMDPR 1387 bp DNA linear PRI 07-NOV-1994  
 DEFINITION Human Duchenne muscular dystrophy gene, exon 1.

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150539\_us-10-539-178-187.rge.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1260 Seconds  
(without alignments)  
1429.452 Million cell updates/sec

Title: US-10-539-178-187

Perfect score: 22

Sequence: 1 cactgtgctattctggtttggaa 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_env:  
2: gb\_pat:  
3: gb\_ph:  
4: gb\_pl:  
5: gb\_pr:  
6: gb\_ro:  
7: gb\_sts:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vi:  
11: gb\_ov:  
12: gb\_in:  
13: gb\_om:  
14: gb\_ba:  
15: gb\_htg1:

16: gb\_htg2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	22	100.0	616	5	AF213401 Homo sapi
	2	22	100.0	1387	5	M32058 Human Duche
	3	22	100.0	11747	5	AF276053 Homo sapi
c	4	22	100.0	133889	5	AL031643 Homo sapi
c	5	22	100.0	185393	5	CR956355 Pan trogl
	6	20.4	92.7	470	6	M86232 Mouse dystro
	7	20.4	92.7	927	6	D83217 Mus musculu
	8	20.4	92.7	110000	16	BX294176 Mus muscu
c	9	20.4	92.7	158789	16	AC154120 Mus muscu
	10	20.4	92.7	237321	6	AL731776 Mouse DNA
	11	19.4	88.2	147851	16	AC170035 Muntiacus
	12	19.4	88.2	156728	16	AC170044 Muntiacus
	13	19.4	88.2	173410	15	AC115330 Rattus no
	14	19.4	88.2	188533	16	AC168950 Muntiacus
c	15	19.4	88.2	220171	15	AC113111 Mus muscu
c	16	19.4	88.2	225302	6	AC109205 Mus muscu
	17	19.4	88.2	227631	15	AC108564 Rattus no
	18	19	86.4	209920	15	AC073682 Mus muscu
	19	18.8	85.5	468	6	M86233 Rat dystrop
c	20	18.8	85.5	107109	5	AL118522 Human DNA
	21	18.8	85.5	110000	14	Continuation (9 of
	22	18.8	85.5	110000	14	Continuation (8 of
c	23	18.8	85.5	150005	5	AL450344 Human DNA
c	24	18.8	85.5	173568	16	AC190427 Cavia por
c	25	18.8	85.5	178481	16	CU464155 Sus scrof
	26	18.8	85.5	187152	16	AC162007 Bos tauru
c	27	18.8	85.5	190535	16	AC153735 Chloroceb
c	28	18.8	85.5	197337	16	CU466241 Sus scrof
c	29	18.8	85.5	208088	16	AC169143 Callicebu
c	30	18.8	85.5	229264	15	AC131219 Rattus no
c	31	18.8	85.5	231767	15	AC094531 Rattus no
	32	18.8	85.5	234588	15	AC103209 Rattus no
	33	18.8	85.5	235718	16	AC162337 Bos tauru
	34	18.8	85.5	236874	15	AC115267 Rattus no
	35	18.4	83.6	2902	4	X83077 Z.mays Fer2
	36	18.4	83.6	40383	6	AC167120 Mus muscu
	37	18.4	83.6	43020	6	AC169082 Mus muscu
	38	18.4	83.6	52568	5	AC093702 Homo sapi
c	39	18.4	83.6	178218	15	AC016841 Homo sapi
	40	18.4	83.6	195003	6	AL731871 Mouse DNA
	41	18.4	83.6	211442	15	AC109502 Mus muscu
c	42	18	81.8	163648	15	AC142370 Rattus no
	43	18	81.8	198211	15	AC073756 Mus muscu
	44	18	81.8	224227	15	AC106509 Rattus no
	45	18	81.8	256059	15	AC098893 Rattus no

## ALIGNMENTS

# **SCORE Search Results Details for Application 10**

## **Result 20080109\_150539\_us-10-539-1**

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This page gives you Search Results detail for the Application 10539178 and Search Result 20080109\_150539\_us-10-539-1.

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1374 Seconds  
(without alignments)  
1429.452 Million cell updates/sec

Title: US-10-539-178-188

Perfect score: 24

Sequence: 1 tttatgcttcttgcaaactactg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_env:  
2: gb\_pat:  
3: gb\_ph:  
4: gb\_pl:  
5: gb\_pr:  
6: gb\_ro:  
7: gb\_sts:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vi:  
11: gb\_ov:  
12: gb\_in:  
13: gb\_om:  
14: gb\_ba:  
15: gb\_htg1:  
16: gb\_htg2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
c 1	24	100.0	1387	5	HUMMDMDPR	M32058 Human Duchenne
c 2	24	100.0	11747	5	AF276053S1	AF276053 Homo sapi
3	24	100.0	133889	5	AL031643	AL031643 Human DNA
4	24	100.0	185393	5	CR956355	CR956355 Pan troglodytes
5	22.4	93.3	211662	5	AL391825	AL391825 Human DNA
c 6	20.8	86.7	160282	16	AC167490	AC167490 Bos taurus
c 7	20.4	85.0	77948	15	AC018982	AC018982 Homo sapi
8	20.4	85.0	153562	5	AC009046	AC009046 Homo sapi
c 9	20.4	85.0	168172	5	AC010528	AC010528 Homo sapi
10	20.4	85.0	188557	15	AC106737	AC106737 Homo sapi
11	20.4	85.0	253694	15	AC084005	AC084005 Homo sapi
12	19.8	82.5	74459	5	BS000616	BS000616 Pan troglodytes
c 13	19.8	82.5	87804	15	AC139126	AC139126 Mus musculus
c 14	19.8	82.5	110000	14	CU207366_21	Continuation (22 o)
c 15	19.8	82.5	150348	6	AC154699	AC154699 Mus musculus
c 16	19.8	82.5	169254	5	AC148934	AC148934 Pan troglodytes
c 17	19.8	82.5	173589	6	CT030695	CT030695 Mouse DNA
c 18	19.8	82.5	182377	6	AC127268	AC127268 Mus musculus
19	19.8	82.5	191701	15	AC080189	AC080189 Homo sapi
20	19.8	82.5	204742	16	AC172902	AC172902 Bos taurus
c 21	19.8	82.5	205053	5	AC011749	AC011749 Homo sapi
22	19.8	82.5	214853	16	AC174691	AC174691 Bos taurus
23	19.8	82.5	218340	15	AC110129	AC110129 Rattus norvegicus
24	19.4	80.8	72137	5	AL356795	AL356795 Human DNA
25	19.4	80.8	115866	5	AL627422	AL627422 Human DNA
c 26	19.4	80.8	177646	15	AC149257	AC149257 Papio anubis
27	19.4	80.8	184461	16	AC188978	AC188978 Zea mays
c 28	19.4	80.8	206089	16	CU407095	CU407095 Sus scrofa
c 29	19.4	80.8	210940	16	AC197143	AC197143 Zea mays
c 30	19.2	80.0	620	7	BV307797	BV307797 S236P6201
c 31	19.2	80.0	630	4	AK250724	AK250724 Hordeum vulgare
32	19.2	80.0	1493	5	AK026202	AK026202 Homo sapi
33	19.2	80.0	2970	2	CS033468	CS033468 Sequence
34	19.2	80.0	2970	2	CS042420	CS042420 Sequence
35	19.2	80.0	2970	5	BC040968	BC040968 Homo sapi
36	19.2	80.0	3679	4	AB164319	AB164319 Bryopsis
37	19.2	80.0	12944	5	DQ418808	DQ418808 Homo sapi
c 38	19.2	80.0	20230	4	AM449533	AM449533 Vitis vinifera
39	19.2	80.0	52813	11	CU459123	CU459123 Zebrafish
c 40	19.2	80.0	76351	11	BX957329	BX957329 Zebrafish
41	19.2	80.0	90139	16	AC174600	AC174600 Strongyloides
42	19.2	80.0	110000	4	AP008208_128	Continuation (129 o)
c 43	19.2	80.0	110000	4	AP008210_182	Continuation (183 o)
c 44	19.2	80.0	110000	14	CP000423_15	Continuation (16 o)
45	19.2	80.0	110000	14	AE017194_16	Continuation (17 o)

## ALIGNMENTS

## RESULT 1

HUMMDMDPR/c

LOCUS HUMMDMDPR 1387 bp DNA linear PRI 07-NOV-1994  
 DEFINITION Human Duchenne muscular dystrophy gene, exon 1.

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150539\_us-10-539-178-2.rge.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1374 Seconds  
(without alignments)  
1429.452 Million cell updates/sec

Title: US-10-539-178-2

Perfect score: 24

Sequence: 1 tcatgtgttagttctatcgcaaa 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_env:  
2: gb\_pat:  
3: gb\_ph:  
4: gb\_pl:  
5: gb\_pr:  
6: gb\_ro:  
7: gb\_sts:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vi:  
11: gb\_ov:  
12: gb\_in:  
13: gb\_om:  
14: gb\_ba:  
15: gb\_htgl:

16: gb\_htg2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
c 1	24	100.0	1387	5	HUMMDPDR	M32058 Human Duche
c 2	24	100.0	11747	5	AF276053S1	AF276053 Homo' sapi
3	24	100.0	133889	5	AL031643	AL031643 Human DNA
4	24	100.0	185393	5	CR956355	CR956355 Pan trogl
c 5	20.8	86.7	29554	4	AM432735	AM432735 Vitis vin
c 6	20.4	85.0	206472	15	AC126091	AC126091 Rattus no
7	19.4	80.8	171795	16	AC202651	AC202651 Nomascus
c 8	19.4	80.8	184786	5	AC198612	AC198612 Pongo pyg
9	19.4	80.8	203832	5	AC198040	AC198040 Pongo pyg
10	19.2	80.0	121639	16	AC177296	AC177296 Strongylo
c 11	19.2	80.0	160626	16	AC181464	AC181464 Strongylo
c 12	19.2	80.0	164119	16	CU329691	CU329691 Sus scrof
c 13	19.2	80.0	169464	16	AC180025	AC180025 Strongylo
c 14	19.2	80.0	170373	16	AC178677	AC178677 Strongylo
c 15	19.2	80.0	218427	6	AL645727	AL645727 Mouse DNA
16	19.2	80.0	220992	16	AC180045	AC180045 Strongylo
17	19.2	80.0	246025	16	AC202299	AC202299 Medicago
c 18	19.2	80.0	257850	16	AC163552	AC163552 Bos tauru
19	18.8	78.3	110000	4	CR382139_02	Continuation (3 of
20	18.8	78.3	110000	4	CR382139_03	Continuation (4 of
21	18.8	78.3	153938	16	AC168572	AC168572 Strongylo
c 22	18.8	78.3	182110	15	AC027466	AC027466 Homo sapi
c 23	18.8	78.3	198687	5	AC093298	AC093298 Homo sapi
c 24	18.8	78.3	199133	11	BX323062	BX323062 Zebrafish
c 25	18.4	76.7	3016	4	AM473681	AM473681 Vitis vin
26	18.4	76.7	3285	4	AM465910	AM465910 Vitis vin
c 27	18.4	76.7	68368	4	AM461419	AM461419 Vitis vin
c 28	18.4	76.7	165705	11	AL929074	AL929074 Zebrafish
29	18.4	76.7	221953	15	AC130078	AC130078 Rattus no
30	18.4	76.7	270120	15	AC128627	AC128627 Rattus no
c 31	18.2	75.8	1107	11	DQ018673	DQ018673 Plethodon
32	18.2	75.8	3707	14	AF047839	AF047839 Pseudoalt
33	18.2	75.8	6153	5	CR627432	CR627432 Homo sapi
c 34	18.2	75.8	9894	11	AJ867256	AJ867256 Oncorhync
c 35	18.2	75.8	28538	15	AC023735	AC023735 Drosophil
c 36	18.2	75.8	35383	12	U41510	U41510 Caenorhabdi
c 37	18.2	75.8	71066	16	CT009626_3	Continuation (4 of
38	18.2	75.8	101319	5	AL392109	AL392109 Human DNA
c 39	18.2	75.8	110000	16	CT009626_1	Continuation (2 of
c 40	18.2	75.8	134375	16	AC178147	AC178147 Strongylo
41	18.2	75.8	138302	16	CU075371	CU075371 Sus scrof
42	18.2	75.8	148101	16	AC199691	AC199691 Spermophi
43	18.2	75.8	149039	15	AC143506	AC143506 Macaca mu
c 44	18.2	75.8	151707	6	AC193858	AC193858 Mus muscu
c 45	18.2	75.8	155370	16	AC155783	AC155783 Papio anu

## ALIGNMENTS

# **SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150548\_us-10-539-178-1.rni.**

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:31:44 ; Search time 266 Seconds  
(without alignments)  
295.437 Million cell updates/sec

Title: US-10-539-178-1  
Perfect score: 20  
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5378416 seqs, 1963011933 residues

Total number of hits satisfying chosen parameters: 10756832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
 1: /ABSS/Data/CRF/ptodata/2/ina/1\_COMB.seq:  
 2: /ABSS/Data/CRF/ptodata/2/ina/5\_COMB.seq:  
 3: /ABSS/Data/CRF/ptodata/2/ina/6A\_COMB.seq:  
 4: /ABSS/Data/CRF/ptodata/2/ina/6B\_COMB.seq:  
 5: /ABSS/Data/CRF/ptodata/2/ina/7A\_COMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	16.8	84.0	453	7	US-09-925-065A-222523	Sequence 222523,
5	16.8	84.0	453	7	US-09-925-065A-222524	Sequence 222524,
c 6	16.8	84.0	471	7	US-09-925-065A-569405	Sequence 569405,
c 7	16.8	84.0	476	7	US-09-925-065A-110478	Sequence 110478,
c 8	16.8	84.0	482	7	US-09-925-065A-817635	Sequence 817635,
c 9	16.8	84.0	487	7	US-09-925-065A-739090	Sequence 739090,
c 10	16.8	84.0	528	7	US-09-925-065A-906486	Sequence 906486,
c 11	16.8	84.0	533	7	US-09-925-065A-784229	Sequence 784229,
c 12	16.8	84.0	540	7	US-09-925-065A-180903	Sequence 180903,
c 13	16.8	84.0	540	7	US-09-925-065A-180904	Sequence 180904,
c 14	16.8	84.0	540	7	US-09-925-065A-180905	Sequence 180905,
c 15	16.8	84.0	574	7	US-09-925-065A-891843	Sequence 891843,
c 16	16.8	84.0	594	7	US-09-925-065A-311114	Sequence 311114,
c 17	16.8	84.0	599	7	US-09-925-065A-572287	Sequence 572287,
18	16.8	84.0	602	7	US-09-925-065A-444385	Sequence 444385,
c 19	16.8	84.0	607	7	US-09-925-065A-530004	Sequence 530004,
20	16.8	84.0	631	7	US-09-925-065A-395574	Sequence 395574,
21	16.8	84.0	631	7	US-09-925-065A-395575	Sequence 395575,
c 22	16.8	84.0	631	7	US-09-925-065A-938412	Sequence 938412,
c 23	16.8	84.0	631	7	US-09-925-065A-938413	Sequence 938413,
24	16.8	84.0	669	7	US-09-925-065A-907607	Sequence 907607,
c 25	16.8	84.0	670	7	US-09-925-065A-877462	Sequence 877462,
c 26	16.8	84.0	670	7	US-09-925-065A-906281	Sequence 906281,
27	16.8	84.0	725	7	US-09-925-065A-717833	Sequence 717833,
28	16.8	84.0	771	7	US-09-925-065A-939969	Sequence 939969,
29	16.8	84.0	16922	3	US-09-949-002-671	Sequence 671, App
30	16.8	84.0	16923	3	US-09-949-002-708	Sequence 708, App
c 31	16.4	82.0	449	7	US-09-925-065A-880454	Sequence 880454,
32	16.4	82.0	455	7	US-09-925-065A-870559	Sequence 870559,
c 33	16.4	82.0	554	7	US-09-925-065A-201120	Sequence 201120,
34	16.4	82.0	563	7	US-09-925-065A-190081	Sequence 190081,
c 35	16.4	82.0	568	7	US-09-925-065A-599747	Sequence 599747,
c 36	16.4	82.0	576	7	US-09-925-065A-415796	Sequence 415796,
c 37	16.4	82.0	601	3	US-09-949-016-96596	Sequence 96596, A
c 38	16.4	82.0	601	3	US-09-949-016-96597	Sequence 96597, A
c 39	16.4	82.0	601	3	US-09-949-016-96862	Sequence 96862, A
c 40	16.4	82.0	601	3	US-09-949-016-96863	Sequence 96863, A
c 41	16.4	82.0	601	3	US-09-949-016-97128	Sequence 97128, A
c 42	16.4	82.0	601	3	US-09-949-016-97129	Sequence 97129, A
c 43	16.4	82.0	601	3	US-09-949-016-97394	Sequence 97394, A
c 44	16.4	82.0	601	3	US-09-949-016-97395	Sequence 97395, A
c 45	16.4	82.0	601	3	US-09-949-016-97660	Sequence 97660, A

## ALIGNMENTS

## RESULT 1

US-09-949-016-12017/c  
; Sequence 12017, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150548\_us-10-539-178-187.rni.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:31:44 ; Search time 292 Seconds  
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295.437 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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c 4	17.8	80.9	2956	7	US-09-925-065A-686160	Sequence 686160,
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c 6	17.4	79.1	163662	3	US-09-949-016-12545	Sequence 12545, A
c 7	17.4	79.1	163664	3	US-09-949-016-13546	Sequence 13546, A
8	17.2	78.2	561	7	US-09-925-065A-563013	Sequence 563013,
9	17.2	78.2	562	7	US-09-925-065A-395750	Sequence 395750,
10	17.2	78.2	594	5	US-10-703-032-81796	Sequence 81796, A
11	17.2	78.2	601	3	US-09-949-016-53876	Sequence 53876, A
c 12	17.2	78.2	614	7	US-09-925-065A-418559	Sequence 418559,
c 13	17.2	78.2	632	7	US-09-925-065A-93681	Sequence 93681, A
c 14	17.2	78.2	700	3	US-09-735-271-1113	Sequence 1113, Ap
15	17.2	78.2	2335	3	US-10-104-047-704	Sequence 704, App
16	17.2	78.2	75176	3	US-09-949-016-13300	Sequence 13300, A
c 17	17.2	78.2	187136	3	US-09-949-016-17231	Sequence 17231, A
18	17.2	78.2	360470	3	US-09-949-016-13173	Sequence 13173, A
c 19	16.8	76.4	547	7	US-09-925-065A-767437	Sequence 767437,
c 20	16.8	76.4	597	7	US-09-925-065A-748035	Sequence 748035,
c 21	16.8	76.4	608	7	US-09-925-065A-367436	Sequence 367436,
c 22	16.8	76.4	608	7	US-09-925-065A-786198	Sequence 786198,
c 23	16.8	76.4	608	7	US-09-925-065A-786199	Sequence 786199,
c 24	16.8	76.4	613	7	US-09-925-065A-833516	Sequence 833516,
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c 26	16.8	76.4	617	7	US-09-925-065A-348909	Sequence 348909,
c 27	16.8	76.4	634	7	US-09-925-065A-882797	Sequence 882797,
28	16.8	76.4	636	7	US-09-925-065A-356508	Sequence 356508,
29	16.8	76.4	636	7	US-09-925-065A-356509	Sequence 356509,
c 30	16.8	76.4	658	7	US-09-925-065A-806242	Sequence 806242,
c 31	16.8	76.4	659	7	US-09-925-065A-806236	Sequence 806236,
c 32	16.8	76.4	665	7	US-09-925-065A-748036	Sequence 748036,
c 33	16.8	76.4	667	7	US-09-925-065A-806740	Sequence 806740,
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35	16.8	76.4	726	7	US-09-925-065A-765539	Sequence 765539,
c 36	16.8	76.4	815	7	US-09-925-065A-7264	Sequence 7264, Ap
37	16.8	76.4	1431	7	US-09-925-065A-682858	Sequence 682858,
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c 39	16.8	76.4	162025	3	US-09-834-700-13	Sequence 13, Appl
c 40	16.8	76.4	162025	3	US-09-834-700-14	Sequence 14, Appl
c 41	16.8	76.4	162025	3	US-09-834-700-17	Sequence 17, Appl
c 42	16.8	76.4	162025	3	US-09-834-700-18	Sequence 18, Appl
43	16.4	74.5	4267	3	US-09-023-655-1379	Sequence 1379, Ap
44	16.4	74.5	110243	3	US-09-949-016-13698	Sequence 13698, A
c 45	16.4	74.5	146428	3	US-09-949-016-12620	Sequence 12620, A

## ALIGNMENTS

## RESULT 1

US-09-925-065A-914264/c

; Sequence 914264, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

# **SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150548\_us-10-539-178-188.rni.**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	22.4	93.3	197132	3	US-09-949-016-17170		Sequence 17170, A
4	20.4	85.0	523	7	US-09-925-065A-24021		Sequence 24021, A
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c 6	19.2	80.0	464	7	US-09-925-065A-810864		Sequence 810864,
7	19.2	80.0	538	7	US-09-925-065A-658760		Sequence 658760,
c 8	19.2	80.0	756	7	US-09-925-065A-686845		Sequence 686845,
c 9	18.4	76.7	695	7	US-09-925-065A-84644		Sequence 84644, A
c 10	18.4	76.7	1578	3	US-08-956-171E-216		Sequence 216, App
c 11	18.4	76.7	1578	3	US-08-781-986A-216		Sequence 216, App
12	18.2	75.8	484	7	US-09-925-065A-104009		Sequence 104009,
13	18.2	75.8	484	7	US-09-925-065A-104010		Sequence 104010,
14	18.2	75.8	484	7	US-09-925-065A-104011		Sequence 104011,
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16	18.2	75.8	524	7	US-09-925-065A-620540		Sequence 620540,
17	18.2	75.8	541	7	US-09-925-065A-369884		Sequence 369884,
18	18.2	75.8	594	7	US-09-925-065A-950660		Sequence 950660,
c 19	18.2	75.8	601	3	US-09-949-016-141435		Sequence 141435,
20	18.2	75.8	617	7	US-09-925-065A-863151		Sequence 863151,
c 21	18.2	75.8	675	3	US-09-248-796A-7451		Sequence 7451, Ap
22	18.2	75.8	1473	7	US-09-925-065A-715341		Sequence 715341,
23	18.2	75.8	1473	7	US-09-925-065A-715342		Sequence 715342,
24	18.2	75.8	236964	3	US-09-949-016-15753		Sequence 15753, A
25	17.8	74.2	578	7	US-09-925-065A-618175		Sequence 618175,
26	17.8	74.2	578	7	US-09-925-065A-618176		Sequence 618176,
c 27	17.8	74.2	604	7	US-09-925-065A-760527		Sequence 760527,
c 28	17.8	74.2	610	7	US-09-925-065A-772349		Sequence 772349,
c 29	17.8	74.2	644	7	US-09-925-065A-771937		Sequence 771937,
c 30	17.8	74.2	646	7	US-09-925-065A-836520		Sequence 836520,
31	17.8	74.2	2655	5	US-10-108-260A-1165		Sequence 1165, Ap
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33	17.8	74.2	3383	3	US-09-479-862-12		Sequence 12, Appl
34	17.8	74.2	11464	3	US-08-884-324-13		Sequence 13, Appl
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36	17.8	74.2	11464	3	US-10-100-057-17		Sequence 13, Appl
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38	17.8	74.2	24804	3	US-09-949-016-16377		Sequence 16377, A
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c 44	17.6	73.3	579	7	US-09-925-065A-731104		Sequence 731104,
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## ALIGNMENTS

## RESULT 1

US-09-949-016-189725

; Sequence 189725, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

# SCORE Search Results Details for Application 10539178

## Search Result 20080109\_150548\_us-10-539

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Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	17.6	73.3	603	7	Sequence 362509,
	6	17.6	73.3	603	7	Sequence 362510,
	7	17.6	73.3	645	3	Sequence 627, App
c 8	17.6	73.3	700	7	US-09-925-065A-920970	Sequence 920970,
	9	17.6	73.3	705	7	Sequence 921655,
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c 11	17.6	73.3	1632	3	US-10-046-232-21	Sequence 21, Appl
c 12	17.6	73.3	1632	5	US-10-940-954-21	Sequence 21, Appl
c 13	17.6	73.3	2162	3	US-10-046-232-19	Sequence 19, Appl
c 14	17.6	73.3	2162	5	US-10-940-954-19	Sequence 19, Appl
	15	17.6	73.3	3172	3	Sequence 400, App
	16	17.6	73.3	3817	3	Sequence 5552, Ap
	17	17.6	73.3	3835	3	Sequence 1067, Ap
	18	17.6	73.3	27236	3	Sequence 12809, A
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c 22	17.2	71.7	599	7	US-09-925-065A-342808	Sequence 342808,
c 23	17.2	71.7	599	7	US-09-925-065A-342809	Sequence 342809,
	24	17.2	71.7	603	7	Sequence 640091,
c 25	17.2	71.7	617	7	US-09-925-065A-761196	Sequence 761196,
c 26	17.2	71.7	618	7	US-09-925-065A-754837	Sequence 754837,
c 27	17.2	71.7	629	7	US-09-925-065A-255332	Sequence 255332,
c 28	17.2	71.7	629	7	US-09-925-065A-255333	Sequence 255333,
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	30	17.2	71.7	15051	5	Sequence 172, App
	31	17	70.8	24221	3	Sequence 14964, A
	32	16.8	70.0	513	7	Sequence 625641,
c 33	16.8	70.0	606	7	US-09-925-065A-314732	Sequence 314732,
c 34	16.8	70.0	632	7	US-09-925-065A-793171	Sequence 793171,
c 35	16.8	70.0	651	7	US-09-925-065A-788332	Sequence 788332,
c 36	16.8	70.0	651	7	US-09-925-065A-846702	Sequence 846702,
c 37	16.8	70.0	651	7	US-09-925-065A-846703	Sequence 846703,
c 38	16.8	70.0	232024	3	US-09-949-016-13477	Sequence 13477, A
c 39	16.6	69.2	24	6	US-10-310-914B-840272	Sequence 840272,
	40	16.6	69.2	555	7	Sequence 164065,
	41	16.6	69.2	555	7	Sequence 164066,
c 42	16.6	69.2	582	7	US-09-925-065A-271253	Sequence 271253,
c 43	16.6	69.2	582	7	US-09-925-065A-271254	Sequence 271254,
c 44	16.6	69.2	602	7	US-09-925-065A-147917	Sequence 147917,
c 45	16.6	69.2	602	7	US-09-925-065A-147918	Sequence 147918,

## ALIGNMENTS

## RESULT 1

US-09-949-016-16515/c  
; Sequence 16515, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150553\_us-10-539-178-1.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:35:15 ; Search time 2144 Seconds  
(without alignments)  
233.030 Million cell updates/sec

Title: US-10-539-178-1  
Perfect score: 20  
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34378780 seqs, 12487843900 residues

Total number of hits satisfying chosen parameters: 68757560

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	4	18.4	92.0	377	13	US-10-301-480-615568	Sequence 615568,
c	5	18.4	92.0	397	26	US-11-497-489A-9885	Sequence 9885, Ap
c	6	18.4	92.0	430	13	US-10-301-480-2271	Sequence 2271, Ap
c	7	18.4	92.0	430	13	US-10-301-480-615680	Sequence 615680,
c	8	18.4	92.0	478	26	US-11-497-489A-236963	Sequence 236963,
c	9	18.4	92.0	886	7	US-10-027-632-2657	Sequence 2657, Ap
c	10	18.4	92.0	886	8	US-10-027-632-2657	Sequence 2657, Ap
	11	18.4	92.0	956	13	US-10-301-480-533405	Sequence 533405,
	12	18.4	92.0	956	13	US-10-301-480-1146814	Sequence 1146814,
c	13	18.4	92.0	85869	16	US-10-940-774-12017	Sequence 12017, A
c	14	18.4	92.0	85878	16	US-10-940-774-16321	Sequence 16321, A
c	15	17.4	87.0	315	26	US-11-497-489A-139971	Sequence 139971,
c	16	17.4	87.0	444	26	US-11-497-489A-168595	Sequence 168595,
c	17	17.4	87.0	471	26	US-11-497-489A-168427	Sequence 168427,
c	18	17.4	87.0	611	4	US-09-925-065A-626421	Sequence 626421,
c	19	17.4	87.0	611	5	US-09-925-065A-626421	Sequence 626421,
	20	17.4	87.0	101365	10	US-10-719-993-6830	Sequence 6830, Ap
	21	17.4	87.0	172781	20	US-11-112-908-25	Sequence 25, Appli
c	22	17	85.0	1188	11	US-10-750-185-64683	Sequence 64683, A
c	23	17	85.0	1188	11	US-10-750-623-64683	Sequence 64683, A
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	26	16.8	84.0	201	10	US-10-741-600-32177	Sequence 32177, A
	27	16.8	84.0	201	10	US-10-741-600-32392	Sequence 32392, A
	28	16.8	84.0	201	15	US-10-767-471-23710	Sequence 23710, A
	29	16.8	84.0	201	15	US-10-767-471-23713	Sequence 23713, A
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c	32	16.8	84.0	231	26	US-11-497-489A-150660	Sequence 150660,
c	33	16.8	84.0	249	26	US-11-497-489A-45367	Sequence 45367, A
c	34	16.8	84.0	277	26	US-11-497-489A-123526	Sequence 123526,
c	35	16.8	84.0	290	26	US-11-497-489A-7563	Sequence 7563, Ap
	36	16.8	84.0	293	23	US-11-521-349-10419	Sequence 10419, A
	37	16.8	84.0	293	25	US-11-503-243A-431334	Sequence 431334,

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:35:15 ; Search time 2358 Seconds  
(without alignments)  
233.030 Million cell updates/sec

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result		Query					Description
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	2	22	100.0	2300	27	US-11-636-385-43599	Sequence 43599, A
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	5	18.4	83.6	201	16	US-10-990-328-171628	Sequence 171628,
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c	7	18.4	83.6	523	5	US-09-925-065A-457123	Sequence 457123,
c	8	18.4	83.6	540	13	US-10-301-480-515054	Sequence 515054,
c	9	18.4	83.6	540	13	US-10-301-480-1128463	Sequence 1128463,
	10	18.4	83.6	139110	16	US-10-990-328-94076	Sequence 94076, A
	11	17.8	80.9	25	29	US-11-695-599-222923	Sequence 222923,
	12	17.8	80.9	25	29	US-11-695-599-467600	Sequence 467600,
c	13	17.8	80.9	33	24	US-11-406-880B-23795	Sequence 23795, A
c	14	17.8	80.9	472	10	US-10-425-115-173837	Sequence 173837,
c	15	17.8	80.9	700	26	US-11-443-428A-229378	Sequence 229378,
c	16	17.8	80.9	1510	11	US-10-487-901-3616	Sequence 3616, Ap
c	17	17.8	80.9	1510	11	US-10-487-901-7291	Sequence 7291, Ap
	18	17.8	80.9	2805	9	US-10-424-599-47506	Sequence 47506, A
c	19	17.8	80.9	2956	4	US-09-925-065A-686159	Sequence 686159,
c	20	17.8	80.9	2956	4	US-09-925-065A-686160	Sequence 686160,
c	21	17.8	80.9	2956	5	US-09-925-065A-686159	Sequence 686159,
c	22	17.8	80.9	2956	5	US-09-925-065A-686160	Sequence 686160,
	23	17.4	79.1	601	16	US-10-940-774-62517	Sequence 62517, A
c	24	17.4	79.1	163662	16	US-10-940-774-12545	Sequence 12545, A
c	25	17.4	79.1	163664	16	US-10-940-774-13546	Sequence 13546, A
c	26	17.2	78.2	368	25	US-11-486-448-29255	Sequence 29255, A
c	27	17.2	78.2	368	25	US-11-503-243A-238507	Sequence 238507,
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GenCore version 6.2.1  
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233.030 Million cell updates/sec

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Perfect score: 24  
Sequence: 1 tttatgcttcttgcaaactactg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34378780 seqs, 12487843900 residues

Total number of hits satisfying chosen parameters: 68757560

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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#### SUMMARIES

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	4	22.4	.93.3	197131	16	US-10-940-774-12675	Sequence 12675, A
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	10	20.4	85.0	523	5	US-09-925-065A-24021	Sequence 24021, A
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	12	20.4	85.0	523	13	US-10-301-480-738667	Sequence 738667,
	13	19.4	80.8	426	29	US-11-239-625A-1152	Sequence 1152, Ap
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c	15	19.4	80.8	568	4	US-09-925-065A-237168	Sequence 237168,
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	19	19.2	80.0	64	25	US-11-130-645A-429715	Sequence 429715,
c	20	19.2	80.0	464	4	US-09-925-065A-810864	Sequence 810864,
c	21	19.2	80.0	464	5	US-09-925-065A-810864	Sequence 810864,
	22	19.2	80.0	538	4	US-09-925-065A-658760	Sequence 658760,
	23	19.2	80.0	538	5	US-09-925-065A-658760	Sequence 658760,
	24	19.2	80.0	600	11	US-10-972-079-83593	Sequence 83593, A
	25	19.2	80.0	600	11	US-10-972-079-83594	Sequence 83594, A
	26	19.2	80.0	600	11	US-10-972-079-83595	Sequence 83595, A
c	27	19.2	80.0	756	4	US-09-925-065A-686845	Sequence 686845,
c	28	19.2	80.0	756	5	US-09-925-065A-686845	Sequence 686845,
	29	19.2	80.0	1000	21	US-11-266-748A-283981	Sequence 283981,
c	30	19.2	80.0	1000	21	US-11-266-748A-335410	Sequence 335410,
	31	19.2	80.0	1000	21	US-11-266-748A-393829	Sequence 393829,
c	32	19.2	80.0	1000	21	US-11-266-748A-464875	Sequence 464875,
	33	19.2	80.0	1438	26	US-11-443-428A-730445	Sequence 730445,
	34	19.2	80.0	1501	6	US-09-815-264-51827	Sequence 51827, A
	35	19.2	80.0	1501	27	US-11-595-983-51827	Sequence 51827, A
	36	19.2	80.0	2218	26	US-11-443-428A-460989	Sequence 460989,
	37	19.2	80.0	2942	25	US-11-433-832-44604	Sequence 44604, A

# SCORE Search Results Details for Application 10539178 and Search Result **20080109\_150553\_us-10-539-178-2.rnpbm.**

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GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:35:15 ; Search time 2572 Seconds  
(without alignments)  
233.030 Million cell updates/sec

Title: US-10-539-178-2

Perfect score: 24

Sequence: 1 tcatgtgttagttatcgcaaa 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34378780 seqs, 12487843900 residues

Total number of hits satisfying chosen parameters: 68757560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:  
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2: /ABSS/Data/CRF/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

3: /ABSS/Data/CRF/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

4: /ABSS/Data/CRF/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

5: /ABSS/Data/CRF/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

6: /ABSS/Data/CRF/ptodata/2/pubpna/US09D\_PUBCOMB.seq:\*

7: /ABSS/Data/CRF/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

8: /ABSS/Data/CRF/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

9: /ABSS/Data/CRF/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

10: /ABSS/Data/CRF/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

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13: /ABSS/Data/CRF/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*

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15: /ABSS/Data/CRF/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*

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17: /ABSS/Data/CRF/ptodata/2/pubpna/US10K_PUBCOMB.seq:*
18: /ABSS/Data/CRF/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
19: /ABSS/Data/CRF/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
20: /ABSS/Data/CRF/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
21: /ABSS/Data/CRF/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
22: /ABSS/Data/CRF/ptodata/2/pubpna/US11E_PUBCOMB.seq:*
23: /ABSS/Data/CRF/ptodata/2/pubpna/US11F_PUBCOMB.seq:*
24: /ABSS/Data/CRF/ptodata/2/pubpna/US11G_PUBCOMB.seq:*
25: /ABSS/Data/CRF/ptodata/2/pubpna/US11H_PUBCOMB.seq:*
26: /ABSS/Data/CRF/ptodata/2/pubpna/US11I_PUBCOMB.seq:*
27: /ABSS/Data/CRF/ptodata/2/pubpna/US11J_PUBCOMB.seq:*
28: /ABSS/Data/CRF/ptodata/2/pubpna/US11K_PUBCOMB.seq:*
29: /ABSS/Data/CRF/ptodata/2/pubpna/US11L_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query					Description
		Match	Length	DB	ID		
1	24	100.0	24	14	US-10-539-178-2		Sequence 2, Appli
c 2	18.2	75.8	302	26	US-11-497-489A-250518		Sequence 250518,
c 3	18.2	75.8	372	26	US-11-497-489A-242942		Sequence 242942,
c 4	18.2	75.8	391	26	US-11-497-489A-142573		Sequence 142573,
c 5	18.2	75.8	393	26	US-11-497-489A-170489		Sequence 170489,
c 6	18.2	75.8	439	26	US-11-497-489A-72756		Sequence 72756, A
c 7	18.2	75.8	624	26	US-11-497-489A-41562		Sequence 41562, A
c 8	18.2	75.8	1039	9	US-10-424-599-90058		Sequence 90058, A
c 9	18.2	75.8	131780	16	US-10-990-328-97256		Sequence 97256, A
c 10	18.2	75.8	163022	16	US-10-940-774-16515		Sequence 16515, A
11	18.2	75.8	191410	16	US-10-990-328-95165		Sequence 95165, A
12	18.2	75.8	221600	11	US-10-840-590-1		Sequence 1, Appli
13	17.8	74.2	1147	23	US-11-491-125A-62465		Sequence 62465, A
14	17.8	74.2	7519	23	US-11-491-125A-50542		Sequence 50542, A
15	17.8	74.2	19332	23	US-11-491-125A-8715		Sequence 8715, Ap
c 16	17.8	74.2	38068	23	US-11-491-125A-16861		Sequence 16861, A
17	17.8	74.2	51472	6	US-09-815-264-81524		Sequence 81524, A
18	17.8	74.2	51472	27	US-11-595-983-81524		Sequence 81524, A
c 19	17.8	74.2	118315	6	US-09-815-264-70214		Sequence 70214, A
c 20	17.8	74.2	118315	27	US-11-595-983-70214		Sequence 70214, A
21	17.6	73.3	64	23	US-11-511-035-448361		Sequence 448361,
22	17.6	73.3	201	16	US-10-990-328-453999		Sequence 453999,
23	17.6	73.3	380	9	US-10-242-535A-16641		Sequence 16641, A
24	17.6	73.3	380	9	US-10-085-783A-16641		Sequence 16641, A
c 25	17.6	73.3	383	27	US-11-486-299A-57799		Sequence 57799, A
26	17.6	73.3	387	26	US-11-497-489A-46515		Sequence 46515, A
27	17.6	73.3	399	3	US-09-918-995-36182		Sequence 36182, A
c 28	17.6	73.3	417	26	US-11-497-489A-185338		Sequence 185338,
c 29	17.6	73.3	443	26	US-11-497-489A-45750		Sequence 45750, A
30	17.6	73.3	507	7	US-10-102-524-1373		Sequence 1373, Ap
31	17.6	73.3	557	26	US-11-443-428A-85105		Sequence 85105, A
32	17.6	73.3	567	4	US-09-925-065A-57825		Sequence 57825, A
33	17.6	73.3	567	5	US-09-925-065A-57825		Sequence 57825, A
34	17.6	73.3	567	13	US-10-301-480-159063		Sequence 159063,
35	17.6	73.3	567	13	US-10-301-480-772472		Sequence 772472,
36	17.6	73.3	600	14	US-10-956-160-215646		Sequence 215646,
37	17.6	73.3	601	14	US-10-956-160-5539		Sequence 5539, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:38:20 ; Search time 4 Seconds  
(without alignments)  
18.095 Million cell updates/sec

Title: US-10-539-178-1  
Perfect score: 20  
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
1: /ABSS/Data/CRF/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
2: /ABSS/Data/CRF/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	%				Description
		Match	Length	DB	ID	
c 1	12.8	64.0	439	1	US-10-959-789-508	Sequence 508, App
c 2	12.8	64.0	762	2	US-11-781-818-63	Sequence 63, Appl
c 3	12.8	64.0	762	2	US-11-781-818-64	Sequence 64, Appl

c	4	12.8	64.0	1242	2	US-11-558-961-5	Sequence 5, Appli
	5	12.6	63.0	277	1	US-10-959-789-2568	Sequence 2568, Ap
c	6	12.6	63.0	1962	2	US-11-801-040-24	Sequence 24, Appl
	7	12.6	63.0	2421	1	US-10-598-073-19	Sequence 19, Appl
	8	12.6	63.0	6016	2	US-11-676-172-3	Sequence 3, Appli
	9	12.6	63.0	9941	2	US-11-683-962-3	Sequence 3, Appli
	10	12.6	63.0	9941	2	US-11-689-407-3	Sequence 3, Appli
	11	12.4	62.0	523	1	US-10-959-789-2687	Sequence 2687, Ap
	12	12.2	61.0	312	1	US-10-959-789-2726	Sequence 2726, Ap
c	13	12.2	61.0	997	2	US-11-801-040-33	Sequence 33, Appl
c	14	12.2	61.0	1568	2	US-11-220-398A-69	Sequence 69, Appl
c	15	12.2	61.0	2128	2	US-11-220-398A-22	Sequence 22, Appl
c	16	12	60.0	71	2	US-11-753-263-78	Sequence 78, Appl
c	17	12	60.0	131	2	US-11-676-985-2	Sequence 2, Appli
c	18	11.8	59.0	96	1	US-10-959-789-909	Sequence 909, App
c	19	11.8	59.0	226	1	US-10-959-789-927	Sequence 927, App
c	20	11.8	59.0	228	1	US-10-959-789-928	Sequence 928, App
c	21	11.8	59.0	263	1	US-10-959-789-924	Sequence 924, App
c	22	11.8	59.0	266	1	US-10-959-789-923	Sequence 923, App
c	23	11.8	59.0	271	1	US-10-959-789-922	Sequence 922, App
c	24	11.8	59.0	293	1	US-10-959-789-2632	Sequence 2632, Ap
c	25	11.8	59.0	300	1	US-10-959-789-921	Sequence 921, App
c	26	11.8	59.0	303	1	US-10-959-789-862	Sequence 862, App
c	27	11.8	59.0	316	1	US-10-959-789-920	Sequence 920, App
	28	11.8	59.0	5289	2	US-11-220-398A-212	Sequence 212, App
c	29	11.6	58.0	67	2	US-11-753-263-52	Sequence 52, Appl
	30	11.6	58.0	221	1	US-10-959-789-758	Sequence 758, App
	31	11.6	58.0	299	1	US-10-959-789-933	Sequence 933, App
c	32	11.6	58.0	489	1	US-10-959-789-930	Sequence 930, App
c	33	11.6	58.0	519	1	US-10-959-789-849	Sequence 849, App
	34	11.6	58.0	1228	2	US-11-801-040-25	Sequence 25, Appl
	35	11.6	58.0	2369	2	US-11-823-707-1	Sequence 1, Appli
	36	11.6	58.0	2369	2	US-11-823-707-2	Sequence 2, Appli
c	37	11.6	58.0	2391	1	US-10-598-073-25	Sequence 25, Appl
c	38	11.6	58.0	6177	2	US-11-668-333-44	Sequence 44, Appl
	39	11.4	57.0	287	1	US-10-959-789-2750	Sequence 2750, Ap
	40	11.4	57.0	298	1	US-10-959-789-2787	Sequence 2787, Ap
c	41	11.4	57.0	571	1	US-10-959-789-464	Sequence 464, App
	42	11.4	57.0	1379	2	US-11-801-040-18	Sequence 18, Appl
c	43	11.4	57.0	6127	2	US-11-401-765-1	Sequence 1, Appli
c	44	11.2	56.0	70	2	US-11-753-263-79	Sequence 79, Appl
c	45	11.2	56.0	70	2	US-11-753-263-241	Sequence 241, App

## ALIGNMENTS

## RESULT 1

US-10-959-789-508/c

; Sequence 508, Application US/10959789

; Publication No. US20080005809A1

; GENERAL INFORMATION:

; APPLICANT: Bledig, Stefan A.

; APPLICANT: Byrum, Joseph R.

; APPLICANT: Liu, Jingdong

; TITLE OF INVENTION: Nucleic Acid molecules And Other Molecules Associated With The

; TITLE OF INVENTION: Methionine Synthesis And Degradation Pathways

; FILE REFERENCE: 16517.328

; CURRENT APPLICATION NUMBER: US/10/959,789

; CURRENT FILING DATE: 2004-10-07

; PRIOR APPLICATION NUMBER: US 09/198,779

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150558\_us-10-539-178-187.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:38:20 ; Search time 5 Seconds  
(without alignments)  
18.095 Million cell updates/sec

Title: US-10-539-178-187  
Perfect score: 22  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
1: /ABSS/Data/CRF/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
2: /ABSS/Data/CRF/ptodata/1/pubpna/US11\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
c 1	14	63.6	2418	2	US-11-617-282-11	Sequence 11, Appl
c 2	13.6	61.8	316	1	US-10-959-789-920	Sequence 920, App
c 3	12.8	58.2	6016	2	US-11-676-172-3	Sequence 3, Appl

c	4	12.6	57.3	1410	2	US-11-495-624-626	Sequence 626, App
c	5	12.6	57.3	1410	2	US-11-495-624-627	Sequence 627, App
c	6	12.6	57.3	8730	2	US-11-668-333-43	Sequence 43, Appl
c	7	12.4	56.4	1953	2	US-11-220-398A-112	Sequence 112, App
c	8	12.4	56.4	2175	2	US-11-220-398A-110	Sequence 110, App
c	9	12.4	56.4	2316	2	US-11-220-398A-116	Sequence 116, App
c	10	12.4	56.4	2538	2	US-11-220-398A-114	Sequence 114, App
c	11	12.4	56.4	3168	2	US-11-684-979-23	Sequence 23, Appl
c	12	12.4	56.4	4854	2	US-11-220-398A-118	Sequence 118, App
c	13	12.4	56.4	5076	2	US-11-220-398A-104	Sequence 104, App
c	14	12.4	56.4	8578	2	US-11-220-398A-120	Sequence 120, App
c	15	12.2	55.5	317	1	US-10-959-789-2425	Sequence 2425, Ap
c	16	12.2	55.5	1730	2	US-11-558-961-7	Sequence 7, Appli
c	17	12.2	55.5	3730	2	US-11-713-291-8	Sequence 8, Appli
c	18	12.2	55.5	7934	2	US-11-713-291-1	Sequence 1, Appli
c	19	12	54.5	180	1	US-10-959-789-2261	Sequence 2261, Ap
c	20	12	54.5	257	1	US-10-959-789-2601	Sequence 2601, Ap
c	21	12	54.5	269	1	US-10-959-789-2593	Sequence 2593, Ap
c	22	12	54.5	274	1	US-10-959-789-2600	Sequence 2600, Ap
c	23	12	54.5	274	1	US-10-959-789-2613	Sequence 2613, Ap
c	24	12	54.5	292	1	US-10-959-789-2583	Sequence 2583, Ap
c	25	12	54.5	294	1	US-10-959-789-2552	Sequence 2552, Ap
c	26	12	54.5	297	1	US-10-959-789-2541	Sequence 2541, Ap
c	27	12	54.5	298	1	US-10-959-789-2553	Sequence 2553, Ap
c	28	12	54.5	298	1	US-10-959-789-2591	Sequence 2591, Ap
c	29	12	54.5	306	1	US-10-959-789-2581	Sequence 2581, Ap
c	30	12	54.5	326	1	US-10-959-789-2533	Sequence 2533, Ap
c	31	12	54.5	343	1	US-10-959-789-2548	Sequence 2548, Ap
c	32	12	54.5	476	1	US-10-959-789-2486	Sequence 2486, Ap
c	33	12	54.5	504	1	US-10-959-789-2492	Sequence 2492, Ap
c	34	12	54.5	1914	2	US-11-801-040-34	Sequence 34, Appl
c	35	11.8	53.6	1692	2	US-11-676-172-9	Sequence 9, Appli
c	36	11.8	53.6	6177	2	US-11-668-333-44	Sequence 44, Appl
c	37	11.6	52.7	189	1	US-10-564-615-44	Sequence 44, Appl
c	38	11.6	52.7	243	1	US-10-959-789-866	Sequence 866, App
c	39	11.6	52.7	249	1	US-10-959-789-344	Sequence 344, App
c	40	11.6	52.7	292	1	US-10-959-789-870	Sequence 870, App
c	41	11.6	52.7	799	2	US-11-835-872-1	Sequence 1, Appli
c	42	11.6	52.7	2391	1	US-10-598-073-25	Sequence 25, Appl
c	43	11.6	52.7	5279	1	US-10-592-066-1	Sequence 1, Appli
c	44	11.6	52.7	6127	2	US-11-401-765-1	Sequence 1, Appli
c	45	11.6	52.7	7934	2	US-11-713-291-1	Sequence 1, Appli

## ALIGNMENTS

## RESULT 1

US-11-617-282-11/c

; Sequence 11, Application US/11617282  
; Publication No. US20080003596A1  
; GENERAL INFORMATION:  
; APPLICANT: AKAHOSHI, EIICHI  
; APPLICANT: YOSHIMURA, SEIKO  
; APPLICANT: ISHIHARA, MITSUKO  
; TITLE OF INVENTION: VECTOR AND METHOD FOR DETECTING THE CHANGE IN TRANSCRIPTION AMC  
; FILE REFERENCE: 301374US  
; CURRENT APPLICATION NUMBER: US/11/617,282  
; CURRENT FILING DATE: 2006-12-28  
; PRIOR APPLICATION NUMBER: JP 2006-000135  
; PRIOR FILING DATE: 2006-01-04

# SCORE Search Results Details for Application 10539178 and Search Result **20080109\_150558\_us-10-539-178-188.rnpbn.**

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:38:20 ; Search time 5 Seconds  
(without alignments)  
18.095 Million cell updates/sec

Title: US-10-539-178-188  
Perfect score: 24  
Sequence: 1 tttatgcttcttgcaaactactg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
1: /ABSS/Data/CRF/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
2: /ABSS/Data/CRF/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
						%	Description
c 1	15.6	65.0	6085	2	US-11-676-172-1		Sequence 1, Appl
	2	14.4	60.0	1390	2	US-11-801-040-20	Sequence 20, Appl
c 3	14.2	59.2	1164	2	US-11-739-739-11		Sequence 11, Appl

c	4	13.8	57.5	1242	2	US-11-558-961-5	Sequence 5, Appli
	5	13.6	56.7	8730	2	US-11-668-333-43	Sequence 43, Appl
	6	13.4	55.8	122	1	US-10-564-615-93	Sequence 93, Appl
c	7	13.2	55.0	5925	2	US-11-676-172-5	Sequence 5, Appli
c	8	13.2	55.0	6016	2	US-11-676-172-3	Sequence 3, Appli
	9	13	54.2	173	1	US-10-564-615-63	Sequence 63, Appl
c	10	13	54.2	334	1	US-10-959-789-2997	Sequence 2997, Ap
c	11	13	54.2	603	1	US-10-594-298-1	Sequence 1, Appli
c	12	13	54.2	2590	2	US-11-781-818-85	Sequence 85, Appl
	13	12.8	53.3	1076	2	US-11-801-040-17	Sequence 17, Appl
c	14	12.8	53.3	4854	2	US-11-220-398A-118	Sequence 118, App
c	15	12.8	53.3	5076	2	US-11-220-398A-104	Sequence 104, App
	16	12.8	53.3	6177	2	US-11-668-333-44	Sequence 44, Appl
c	17	12.8	53.3	8578	2	US-11-220-398A-120	Sequence 120, App
c	18	12.6	52.5	2017	2	US-11-801-040-45	Sequence 45, Appl
c	19	12.6	52.5	2026	2	US-11-801-040-30	Sequence 30, Appl
c	20	12.6	52.5	3048	2	US-11-684-979-13	Sequence 13, Appl
c	21	12.6	52.5	3114	2	US-11-684-979-11	Sequence 11, Appl
c	22	12.6	52.5	3730	2	US-11-713-291-8	Sequence 8, Appli
c	23	12.6	52.5	7934	2	US-11-713-291-1	Sequence 1, Appli
	24	12.4	51.7	214	1	US-10-564-615-34	Sequence 34, Appl
c	25	12.4	51.7	2139	2	US-11-684-979-15	Sequence 15, Appl
c	26	12.2	50.8	165	2	US-11-617-282-7	Sequence 7, Appli
c	27	12.2	50.8	1264	2	US-11-801-040-32	Sequence 32, Appl
c	28	12.2	50.8	1542	1	US-10-590-661-8	Sequence 8, Appli
c	29	12.2	50.8	1542	1	US-10-590-661-10	Sequence 10, Appl
	30	12.2	50.8	3208	2	US-11-220-398A-103	Sequence 103, App
c	31	12.2	50.8	8730	2	US-11-668-333-43	Sequence 43, Appl
c	32	12.2	50.8	9941	2	US-11-683-962-3	Sequence 3, Appli
c	33	12.2	50.8	9941	2	US-11-689-407-3	Sequence 3, Appli
	34	12	50.0	306	1	US-10-959-789-2484	Sequence 2484, Ap
c	35	12	50.0	499	1	US-10-959-789-2665	Sequence 2665, Ap
c	36	12	50.0	811	2	US-11-791-839-6	Sequence 6, Appli
c	37	12	50.0	1169	2	US-11-801-040-11	Sequence 11, Appl
	38	12	50.0	1340	2	US-11-801-040-26	Sequence 26, Appl
c	39	12	50.0	2247	2	US-11-220-398A-37	Sequence 37, Appl
	40	12	50.0	8578	2	US-11-220-398A-120	Sequence 120, App
	41	11.8	49.2	270	1	US-10-959-789-893	Sequence 893, App
	42	11.8	49.2	282	1	US-10-959-789-892	Sequence 892, App
c	43	11.8	49.2	295	1	US-10-959-789-804	Sequence 804, App
	44	11.8	49.2	442	1	US-10-959-789-737	Sequence 737, App
	45	11.8	49.2	489	1	US-10-959-789-2797	Sequence 2797, Ap

## ALIGNMENTS

## RESULT 1

US-11-676-172-1/c

; Sequence 1, Application US/11676172  
; Publication No. US20080004713A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Norimasa  
; APPLICANT: MATSUDA, Hikaru  
; APPLICANT: SAWA, Yoshiki  
; APPLICANT: TAKETANI, Satoshi  
; APPLICANT: MIYAGAWA, Shigeru  
; APPLICANT: YOSHIKAWA, Hideki  
; APPLICANT: ANDO, Wataru  
; TITLE OF INVENTION: SCAFFOLD-FREE SELF-ORGANIZED 3D SYNTHETIC TISSUE  
; FILE REFERENCE: 690128.401C1

# SCORE Search Results Details for Application 10539178 and Search Result 20080109\_150558\_us-10-539-178-2.rnpbn.

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GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:38:20 ; Search time 5 Seconds  
(without alignments)  
18.095 Million cell updates/sec

Title: US-10-539-178-2  
Perfect score: 24  
Sequence: 1 tcatgtgttagttctatcgcaaa 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
1: /ABSS/Data/CRF/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
2: /ABSS/Data/CRF/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	64.2	758	2 US-11-617-282-8	Sequence 8, Appli
2	15.4	64.2	1836	2 US-11-617-282-9	Sequence 9, Appli
3	14.6	60.8	1708	2 US-11-495-624-628	Sequence 628, App

4	14.6	60.8	1708	2	US-11-495-624-629	Sequence 629, App	
5	14.6	60.8	1833	2	US-11-670-902-35	Sequence 35, Appl	
6	14.6	60.8	1836	2	US-11-670-902-13	Sequence 13, Appl	
7	14.6	60.8	1851	2	US-11-670-902-21	Sequence 21, Appl	
8	14.6	60.8	1857	2	US-11-670-902-23	Sequence 23, Appl	
9	14.6	60.8	1862	2	US-11-670-902-27	Sequence 27, Appl	
10	14.6	60.8	1865	2	US-11-670-902-25	Sequence 25, Appl	
11	14.6	60.8	1878	2	US-11-670-902-5	Sequence 5, Appl	
12	14.6	60.8	1884	2	US-11-670-902-19	Sequence 19, Appl	
13	13.4	55.8	1310	2	US-11-801-040-12	Sequence 12, Appl	
14	13	54.2	1707	2	US-11-670-902-33	Sequence 33, Appl	
15	13	54.2	2428	2	US-11-572-719-19	Sequence 19, Appl	
c	16	12.6	52.5	6177	2	US-11-668-333-44	Sequence 44, Appl
	17	12.4	51.7	287	1	US-10-959-789-905	Sequence 905, App
	18	12.4	51.7	1205	1	US-10-590-886-1	Sequence 1, Appl
c	19	12.4	51.7	1836	2	US-11-617-282-9	Sequence 9, Appl
	20	12.4	51.7	2139	2	US-11-684-979-15	Sequence 15, Appl
c	21	12.4	51.7	2274	2	US-11-220-398A-60	Sequence 60, Appl
c	22	12.4	51.7	2727	2	US-11-220-398A-38	Sequence 38, Appl
c	23	12.4	51.7	2961	2	US-11-684-979-9	Sequence 9, Appl
c	24	12.4	51.7	3160	2	US-11-220-398A-62	Sequence 62, Appl
c	25	12.2	50.8	114	2	US-11-495-624-149	Sequence 149, App
c	26	12.2	50.8	114	2	US-11-495-624-150	Sequence 150, App
c	27	12.2	50.8	317	1	US-10-959-789-1645	Sequence 1645, Ap
	28	12	50.0	292	1	US-10-959-789-627	Sequence 627, App
	29	12	50.0	334	1	US-10-959-789-2648	Sequence 2648, Ap
	30	12	50.0	340	1	US-10-959-789-580	Sequence 580, App
	31	12	50.0	6834	2	US-11-849-643-5	Sequence 5, Appl
	32	11.8	49.2	137	1	US-10-564-615-40	Sequence 40, Appl
c	33	11.8	49.2	144	1	US-10-564-615-71	Sequence 71, Appl
	34	11.8	49.2	277	1	US-10-959-789-943	Sequence 943, App
c	35	11.8	49.2	310	1	US-10-959-789-898	Sequence 898, App
c	36	11.8	49.2	454	1	US-10-959-789-897	Sequence 897, App
c	37	11.8	49.2	1431	2	US-11-801-040-21	Sequence 21, Appl
	38	11.8	49.2	1962	2	US-11-801-040-24	Sequence 24, Appl
c	39	11.8	49.2	2476	2	US-11-792-242-6	Sequence 6, Appl
	40	11.8	49.2	3712	2	US-11-684-979-61	Sequence 61, Appl
	41	11.6	48.3	602	1	US-10-959-789-1044	Sequence 1044, Ap
	42	11.6	48.3	2391	1	US-10-598-073-25	Sequence 25, Appl
c	43	11.4	47.5	67	2	US-11-753-263-334	Sequence 334, App
c	44	11.4	47.5	70	2	US-11-753-263-158	Sequence 158, App
c	45	11.4	47.5	103	1	US-10-564-615-124	Sequence 124, App

## ALIGNMENTS

RESULT 1  
 US-11-617-282-8  
 ; Sequence 8, Application US/11617282  
 ; Publication No. US20080003596A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AKAHOSHI, EIICHI  
 ; APPLICANT: YOSHIMURA, SEIKO  
 ; APPLICANT: ISHIHARA, MITSUKO  
 ; TITLE OF INVENTION: VECTOR AND METHOD FOR DETECTING THE CHANGE IN TRANSCRIPTION AMC  
 ; FILE REFERENCE: 301374US  
 ; CURRENT APPLICATION NUMBER: US/11/617,282  
 ; CURRENT FILING DATE: 2006-12-28  
 ; PRIOR APPLICATION NUMBER: JP 2006-000135  
 ; PRIOR FILING DATE: 2006-01-04